

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bard, Jonathan A
Borowsky, Beth
Smith, Kelli E
- (ii) TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 65
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212 278 0400
 - (B) TELEFAX: 212 391 0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 63..1172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTCCAGCC TAGGCGTTCT ACCTGGAAGA ATGCAGGGGC CCAGTACCTA GGACTGAGGA	60
AG ATG GCT GAC ATC CAG AAC ATT TCG CTG GAC AGC CCA GGG AGC GTA	107

Applicants: Jonathan A. Bard et al.
Serial No.: Not Yet Known
Filed: Herewith
Exhibit 2

Met	Ala	Asp	Ile	Gln	Asn	Ile	Ser	Leu	Asp	Ser	Pro	Gly	Ser	Val		
1				5					10					15		
GGG	GCT	GTG	GCA	GTG	CCT	GTG	ATC	TTT	GCC	CTC	ATC	TTC	CTG	TTG	GGC	155
Gly	Ala	Val	Ala	Val	Pro	Val	Ile	Phe	Ala	Leu	Ile	Phe	Leu	Leu	Gly	
				20					25					30		
ATG	GTG	GGC	AAT	GGG	CTG	GTG	TTG	GCT	GTG	CTA	CTG	CAG	CCT	GGC	CCA	203
Met	Val	Gly	Asn	Gly	Leu	Val	Leu	Ala	Val	Leu	Leu	Gln	Pro	Gly	Pro	
			35					40					45			
AGT	GCC	TGG	CAG	GAG	CCA	AGC	AGT	ACC	ACA	GAT	CTC	TTC	ATC	CTC	AAC	251
Ser	Ala	Trp	Gln	Glu	Pro	Ser	Ser	Thr	Thr	Asp	Leu	Phe	Ile	Leu	Asn	
		50					55					60				
TTG	GCC	GTG	GCC	GAC	CTT	TGC	TTC	ATC	CTG	TGC	TGC	GTG	CCC	TTC	CAG	299
Leu	Ala	Val	Ala	Asp	Leu	Cys	Phe	Ile	Leu	Cys	Cys	Val	Pro	Phe	Gln	
	65					70					75					
GCA	GCC	ATC	TAC	ACA	CTG	GAT	GCC	TGG	CTC	TTT	GGG	GCT	TTC	GTG	TGC	347
Ala	Ala	Ile	Tyr	Thr	Leu	Asp	Ala	Trp	Leu	Phe	Gly	Ala	Phe	Val	Cys	
	80				85				90						95	
AAG	ACG	GTA	CAT	CTG	CTC	ATC	TAC	CTC	ACC	ATG	TAT	GCC	AGC	AGC	TTC	395
Lys	Thr	Val	His	Leu	Leu	Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	
			100						105					110		
ACC	CTG	GCG	GCC	GTC	TCC	CTG	GAC	AGG	TAC	CTG	GCT	GTG	CGG	CAC	CCA	443
Thr	Leu	Ala	Ala	Val	Ser	Leu	Asp	Arg	Tyr	Leu	Ala	Val	Arg	His	Pro	
			115					120					125			
CTG	CGC	TCC	AGA	GCC	CTG	CGC	ACC	CCG	CGC	AAC	GCG	CGC	GCC	GCC	GTG	491
Leu	Arg	Ser	Arg	Ala	Leu	Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Ala	Val	
		130					135					140				
GGG	CTC	GTG	TGG	CTG	CTG	GCG	GCT	CTC	TTT	TCC	GCG	CCC	TAC	CTA	AGC	539
Gly	Leu	Val	Trp	Leu	Leu	Ala	Ala	Leu	Phe	Ser	Ala	Pro	Tyr	Leu	Ser	
	145					150					155					
TAT	TAC	GGC	ACG	GTG	CGC	TAC	GGC	GCG	CTC	GAG	CTC	TGC	GTG	CCC	GCT	587
Tyr	Tyr	Gly	Thr	Val	Arg	Tyr	Gly	Ala	Leu	Glu	Leu	Cys	Val	Pro	Ala	
	160				165					170					175	
TGG	GAG	GAC	GCG	CGG	CGG	CGC	GCG	CTG	GAC	GTG	GCC	ACC	TTC	GCC	GCG	635
Trp	Glu	Asp	Ala	Arg	Arg	Arg	Ala	Leu	Asp	Val	Ala	Thr	Phe	Ala	Ala	
			180						185					190		
GGC	TAC	CTG	CTG	CCG	GTG	GCC	GTG	GTG	AGC	CTG	GCC	TAC	GGA	CGC	ACG	683
Gly	Tyr	Leu	Leu	Pro	Val	Ala	Val	Val	Ser	Leu	Ala	Tyr	Gly	Arg	Thr	
			195					200					205			
CTA	TGT	TTC	CTA	TGG	GCC	GCC	GTG	GGT	CCC	GCG	GGC	GCG	GCG	GCA	GCA	731
Leu	Cys	Phe	Leu	Trp	Ala	Ala	Val	Gly	Pro	Ala	Gly	Ala	Ala	Ala	Ala	
		210					215						220			
GAG	GCG	CGC	AGA	CGG	GCG	ACC	GGC	CGG	GCG	GGA	CGC	GCC	ATG	CTG	GCA	779
Glu	Ala	Arg	Arg	Arg	Ala	Thr	Gly	Arg	Ala	Gly	Arg	Ala	Met	Leu	Ala	
	225					230					235					
GTG	GCC	GCG	CTC	TAC	GCG	CTT	TGC	TGG	GGC	CCG	CAC	CAC	GCG	CTC	ATC	827
Val	Ala	Ala	Leu	Tyr	Ala	Leu	Cys	Trp	Gly	Pro	His	His	Ala	Leu	Ile	
	240				245					250					255	

CTC TGC TTC TGG TAC GGC CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC	875
Leu Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala	
260 265 270	
TGT CGC CTG GCC TCG CAC TGC CTC GCC TAC GCC AAC TCC TGC CTT AAC	923
Cys Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn	
275 280 285	
CCG CTC GTC TAC TCG CTC GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC	971
Pro Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg	
290 295 300	
CGC CTG TGG CCC TGC GGC CGT CGC CGC CAC CGC CAC CAC CAC CGC GCT	1019
Arg Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His His Arg Ala	
305 310 315	
CAT CGA GCC CTC CGT CGT GTC CAG CCG GCG TCT TCG GGC CCC GCC GGT	1067
His Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly	
320 325 330 335	
TAT CCC GGC GAC GCC AGG CCT CGT GGT TGG AGT ATG GAG CCC AGA GGG	1115
Tyr Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly	
340 345 350	
GAT GCT CTG CGT GGT GGT GGA GAG ACT AGA CTA ACC CTG TCC CCC AGG	1163
Asp Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg	
355 360 365	
GGA CCT CAA TAACCCTGCC CGCTTGGACT CTGACGTCTG TCAGAATGCC	1212
Gly Pro Gln	
370	
ACCAAGGAAC ATCTAGGGAA CGGCAGTCTC GCCAGGCTCC ACCAAAAAGC AGAAGCAAAG	1272
TTGCAGGG	1280

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly	
1 5 10 15	
Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly Met	
20 25 30	
Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser	
35 40 45	
Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu	
50 55 60	
Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala	
65 70 75 80	

Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys Lys
85 90 95

Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr
100 105 110

Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro Leu
115 120 125

Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly
130 135 140

Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr
145 150 155 160

Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp
165 170 175

Glu Asp Ala Arg Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly
180 185 190

Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu
195 200 205

Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Glu
210 215 220

Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val
225 230 235 240

Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile Leu
245 250 255

Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys
260 265 270

Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro
275 280 285

Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg
290 295 300

Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His His Arg Ala His
305 310 315 320

Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly Tyr
325 330 335

Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly Asp
340 345 350

Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg Gly
355 360 365

Pro Gln
370

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1417 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAC TCA GCG ATG ACT TTG GCT CTG CTC TCC CCT CCT CCA TCT CCC ACG	48
His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Ser Pro Thr	
375 380 385	
AGC TTC CAG CCC AGA ACA CCT GGC CAG ACC CAG GTC GGG GGA GTT AGA	96
Ser Phe Gln Pro Arg Thr Pro Gly Gln Thr Gln Val Gly Gly Val Arg	
390 395 400	
TCC CGG GGT CAA GCA ACC AGA ACT GGG GGC TCT TGC CTG AGG ATT CCA	144
Ser Arg Gly Gln Ala Thr Arg Thr Gly Gly Ser Cys Leu Arg Ile Pro	
405 410 415	
GCT TCT CTT CCC AGG TGC CCG TCT GAT GGG GAG ATG GCT GAT GCC CAG	192
Ala Ser Leu Pro Arg Cys Pro Ser Asp Gly Glu Met Ala Asp Ala Gln	
420 425 430	
AAC ATT TCA CTG GAC AGC CCA GGG AGT GTG GGG GCC GTG GCA GTG CCT	240
Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly Ala Val Ala Val Pro	
435 440 445 450	
GTG GTC TTT GCC CTA ATC TTC CTG CTG GGC ACA GTG GGC AAT GGG CTG	288
Val Val Phe Ala Leu Ile Phe Leu Leu Gly Thr Val Gly Asn Gly Leu	
455 460 465	
GTG CTG GCA GTG CTC CTG CAG CCT GGC CCG AGT GCC TGG CAG GAG CCT	336
Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser Ala Trp Gln Glu Pro	
470 475 480	
GGC AGC ACC ACG GAC CTG TTC ATC CTC AAC CTG GCG GTG GCT GAC CTC	384
Gly Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu Ala Val Ala Asp Leu	
485 490 495	
TGC TTC ATC CTG TGC TGC GTG CCC TTC CAG GCC ACC ATC TAC ACG CTG	432
Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala Thr Ile Tyr Thr Leu	
500 505 510	
GAT GCC TGG CTC TTT GGG GCC CTC GTC TGC AAG GCC GTG CAC CTG CTC	480
Asp Ala Trp Leu Phe Gly Ala Leu Val Cys Lys Ala Val His Leu Leu	
515 520 525 530	
ATC TAC CTC ACC ATG TAC GCC AGC AGC TTT ACG CTG GCT GCT GTC TCC	528
Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr Leu Ala Ala Val Ser	
535 540 545	
GTG GAC AGG TAC CTG GCC GTG CGG CAC CCG CTG CGC TCG CGC GCC CTG	576
Val Asp Arg Tyr Leu Ala Val Arg His Pro Leu Arg Ser Arg Ala Leu	
550 555 560	
CGC ACG CCG CGT AAC GCC CGC GCC GCA GTG GGG CTG GTG TGG CTG CTG	624

Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Val	Gly	Leu	Val	Trp	Leu	Leu		
565							570				575					
GCG Ala	GCG Ala	CTC Leu	TTC Phe	TCG Ser	GCG Ala	CCC Pro	TAC Tyr	CTC Leu	AGC Ser	TAC Tyr	TAC Tyr	GGC Gly	ACC Thr	GTG Val	CGC Arg	672
	580					585					590					
TAC Tyr	GGC Gly	GCG Ala	CTG Leu	GAG Glu	CTC Leu	TGC Cys	GTG Val	CCC Pro	GCC Ala	TGG Trp	GAG Glu	GAC Asp	GCG Ala	CGC Arg	CGC Arg	720
595					600					605					610	
CGC Arg	GCC Ala	CTG Leu	GAC Asp	GTG Val	GCC Ala	ACC Thr	TTC Phe	GCT Ala	GCC Ala	GGC Gly	TAC Tyr	CTG Leu	CTG Leu	CCC Pro	GTG Val	768
				615					620					625		
GCT Ala	GTG Val	GTG Val	AGC Ser	CTG Leu	GCC Ala	TAC Tyr	GGG Gly	CGC Arg	ACG Thr	CTG Leu	CGC Arg	TTC Phe	CTG Leu	TGG Trp	GCC Ala	816
			630				635						640			
GCC Ala	GTG Val	GGT Gly	CCC Pro	GCG Ala	GGC Gly	GCG Ala	GCG Ala	GCC Ala	GAG Glu	GCG Ala	CGG Arg	CGG Arg	AGG Arg	GCG Ala		864
		645				650					655					
ACG Thr	GGC Gly	CGC Arg	GCG Ala	GGG Gly	CGC Arg	GCC Ala	ATG Met	CTG Leu	GCG Ala	GTG Val	GCC Ala	GCG Ala	CTC Leu	TAC Tyr	GCG Ala	912
	660					665					670					
CTC Leu	TGC Cys	TGG Trp	GGT Gly	CCG Pro	CAC His	CAC His	GCG Ala	CTC Leu	ATC Ile	CTG Leu	TGC Cys	TTC Phe	TGG Trp	TAC Tyr	GGC Gly	960
675					680					685					690	
CGC Arg	TTC Phe	GCC Ala	TTC Phe	AGC Ser	CCG Pro	GCC Ala	ACC Thr	TAC Tyr	GCC Ala	TGC Cys	CGC Arg	CTG Leu	GCC Ala	TCA Ser	CAC His	1008
				695					700					705		
TGC Cys	CTG Leu	GCC Ala	TAC Tyr	GCC Ala	AAC Asn	TCC Ser	TGC Cys	CTC Leu	AAC Asn	CCG Pro	CTC Leu	GTC Val	TAC Tyr	GCG Ala	CTC Leu	1056
			710					715					720			
GCC Ala	TCG Ser	CGC Arg	CAC His	TTC Phe	CGC Arg	GCG Ala	CGC Arg	TTC Phe	CGC Arg	CGC Arg	CTG Leu	TGG Trp	CCG Pro	TGC Cys	GGC Gly	1104
		725				730						735				
CGC Arg	CGA Arg	CGC Arg	CGC Arg	CAC His	CGT Arg	GCC Ala	CGC Arg	CGC Arg	GCC Ala	TTG Leu	CGT Arg	CGC Arg	GTC Val	CGC Arg	CCC Pro	1152
	740					745					750					
GCG Ala	TCC Ser	TCG Ser	GGC Gly	CCA Pro	CCC Pro	GGC Gly	TGC Cys	CCC Pro	GGA Gly	GAC Asp	GCC Ala	CGG Arg	CCT Pro	AGC Ser	GGG Gly	1200
755					760					765					770	
AGG Arg	CTG Leu	CTG Leu	GCT Ala	GGT Gly	GGC Gly	GGC Gly	CAG Gln	GGC Gly	CCG Pro	GAG Glu	CCC Pro	AGG Arg	GAG Glu	GGA Gly	CCC Pro	1248
				775					780					785		
GTC Val	CAC His	GGC Gly	GGA Gly	GAG Glu	GCT Ala	GCC Ala	CGA Arg	GGA Gly	CCG Pro	GAA Glu	TAAACCCTGC	CGCCTGGACT				1301
			790					795								
CCGCCTGTGT CCGTCTGTCT CACTCCCGTT CTCCGAAGGC GGGACGCCAC CGGGCCAGGG																1361
ATGGGGCAAT GCCACGAGCT CTCTGAGGGG CGTTGAGTGG AG																

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His 1	Ser	Ala	Met	Thr 5	Leu	Ala	Leu	Leu	Ser 10	Pro	Pro	Pro	Ser	Pro 15	Thr
Ser	Phe	Gln	Pro 20	Arg	Thr	Pro	Gly	Gln 25	Thr	Gln	Val	Gly	Gly 30	Val	Arg
Ser	Arg	Gly 35	Gln	Ala	Thr	Arg	Thr 40	Gly	Gly	Ser	Cys	Leu 45	Arg	Ile	Pro
Ala	Ser 50	Leu	Pro	Arg	Cys	Pro 55	Ser	Asp	Gly	Glu	Met 60	Ala	Asp	Ala	Gln
Asn 65	Ile	Ser	Leu	Asp	Ser 70	Pro	Gly	Ser	Val	Gly 75	Ala	Val	Ala	Val	Pro 80
Val	Val	Phe	Ala	Leu 85	Ile	Phe	Leu	Leu	Gly 90	Thr	Val	Gly	Asn	Gly 95	Leu
Val	Leu	Ala	Val 100	Leu	Leu	Gln	Pro	Gly 105	Pro	Ser	Ala	Trp	Gln	Glu	Pro
Gly	Ser	Thr 115	Thr	Asp	Leu	Phe	Ile 120	Leu	Asn	Leu	Ala	Val 125	Ala	Asp	Leu
Cys	Phe 130	Ile	Leu	Cys	Cys	Val 135	Pro	Phe	Gln	Ala	Thr 140	Ile	Tyr	Thr	Leu
Asp 145	Ala	Trp	Leu	Phe	Gly 150	Ala	Leu	Val	Cys	Lys 155	Ala	Val	His	Leu	Leu 160
Ile	Tyr	Leu	Thr	Met 165	Tyr	Ala	Ser	Ser	Phe 170	Thr	Leu	Ala	Ala	Val 175	Ser
Val	Asp	Arg	Tyr 180	Leu	Ala	Val	Arg	His 185	Pro	Leu	Arg	Ser	Arg 190	Ala	Leu
Arg	Thr 195	Pro	Arg	Asn	Ala	Arg	Ala 200	Ala	Val	Gly	Leu	Val 205	Trp	Leu	Leu
Ala 210	Ala	Leu	Phe	Ser	Ala	Pro 215	Tyr	Leu	Ser	Tyr	Tyr 220	Gly	Thr	Val	Arg
Tyr 225	Gly	Ala	Leu	Glu	Leu	Cys 230	Val	Pro	Ala	Trp	Glu 235	Asp	Ala	Arg	Arg 240
Arg	Ala	Leu	Asp	Val 245	Ala	Thr	Phe	Ala	Ala 250	Gly	Tyr	Leu	Leu	Pro 255	Val
Ala	Val	Val 260	Ser	Leu	Ala	Tyr	Gly	Arg 265	Thr	Leu	Arg	Phe	Leu	Trp	Ala 270

Ala Val Gly Pro Ala Gly Ala Ala Ala Glu Ala Arg Arg Arg Ala
 275 280 285

Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val Ala Ala Leu Tyr Ala
 290 295 300

Leu Cys Trp Gly Pro His His Ala Leu Ile Leu Cys Phe Trp Tyr Gly
 305 310 315 320

Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys Arg Leu Ala Ser His
 325 330 335

Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro Leu Val Tyr Ala Leu
 340 345 350

Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg Leu Trp Pro Cys Gly
 355 360 365

Arg Arg Arg Arg His Arg Ala Arg Arg Ala Leu Arg Arg Val Arg Pro
 370 375 380

Ala Ser Ser Gly Pro Pro Gly Cys Pro Gly Asp Ala Arg Pro Ser Gly
 385 390 395 400

Arg Leu Leu Ala Gly Gly Gly Gln Gly Pro Glu Pro Arg Glu Gly Pro
 405 410 415

Val His Gly Gly Glu Ala Ala Arg Gly Pro Glu
 420 425

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
 1 5 10 15

Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn
 20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu
 35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys
 50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp
 65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala
 85 90 95

Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His Tyr

100										105					110				
Phe	Phe	Thr	Val	Ser	Met	Leu	Val	Ser	Ile	Phe	Thr	Leu	Ala	Ala	Met				
		115					120					125							
Ser	Val	Asp	Arg	Tyr	Val	Ala	Ile	Val	His	Ser	Arg	Arg	Ser	Ser	Ser				
		130				135					140								
Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu	Gly	Val	Gly	Phe	Ile	Trp	Ala				
145					150					155					160				
Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr	Tyr	Gln	Arg	Leu	Phe				
				165					170					175					
His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	His	Trp	Pro	Asn	Gln				
			180					185					190						
Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	Gly	Tyr	Leu				
		195				200						205							
Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	Leu	Asn	His				
		210				215					220								
Leu	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	Ala	Ser	Lys				
225					230					235					240				
Lys	Lys	Thr	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	Phe	Gly	Ile				
				245					250					255					
Ser	Trp	Leu	Pro	His	His	Val	Ile	His	Leu	Trp	Ala	Glu	Phe	Gly	Ala				
			260					265					270						
Phe	Pro	Leu	Thr	Pro	Ala	Ser	Phe	Phe	Phe	Arg	Ile	Thr	Ala	His	Cys				
		275					280					285							
Leu	Ala	Tyr	Ser	Asn	Ser	Ser	Val	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Leu				
		290				295					300								
Ser	Glu	Asn	Phe	Arg	Lys	Ala	Tyr	Lys	Gln	Val	Phe	Lys	Cys	Arg	Val				
305					310					315					320				
Cys	Asn	Glu	Ser	Pro	His	Gly	Asp	Ala	Lys	Glu	Lys	Asn	Arg	Ile	Asp				
				325					330					335					
Thr	Pro	Pro	Ser	Thr	Asn	Cys	Thr	His	Val										
			340					345											

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGTACCCCT ATTTTTCGCG CTCATCTTCC TCGTGGGCAC CGTGG

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCACCGCCA GCACCAGCGC GTTGCCCACG GTGCCCACGA GGAAG

45

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGCACCAC CAACCTGTTC ATCCTCAACC TGGGCGTGGC CGACCTGTGT

50

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCCTGGAAA GGCACGCAGC ACAGGATGAA ACACAGGTCG GCCACGCCCA

50

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGCAAGGCT GTTCATTTCC TCATCTTTCT CACTATGCAC GCCAG

45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGACGGCG GCCAGCGTGA AGCTGCTGGC GTGCATAGTG AGAAA

45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACGCGCTGG CCGCCATCGG GCTCATCTGG GGGCTAGCAC TGCTC

45

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGTAGCTCAG GTAGGGCCCC GAGAAGAGCA GTGCTAGCCC CCAGA

45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCCATGGAC CTCTGCACCT TCGTCTTTAG CTACCTGCTG CCAGT

45

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCATAGGTC AGACTGAGGA CTAGCACTGG CAGCAGGTAG CTAAA

45

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCATCATC GTGGCGGTGC TTTTCTGCCT CTGTTGGATG CCCCA

45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACACGCAG AGGATAAGCG CGTGGTGGGG CATCCAACAG AGGCA

45

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTGCGCATC CTTTCACACC TAGTTTCCTA TGCCAACCTC TGTGT

45

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGACCAGAGC GTAAACGATG GGGTTGACAC AGGAGTTGGC ATAGGA

46

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCAGTGAA GGAATGGGA GCGA

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTAGTGTATA AACTGCAGA TGAAGGC

27

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAATGGCT CCGGCAGCCA GGG

23

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

23

TTGCAGAGCA GCGAGCCGAA CAC

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

24

GGCTGACATC CAGAACATTT CGCT

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

24

CAGATGTACC GTCTTGACA CGAA

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

24

CATCTGCTCA TCTACCTCAC CATG

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATAGGAAAC ATAGCGTGCG TCCG

24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTTCTAG AGATCCCTCG ACCTC

25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGCGCAGAA CTGGTAGGTA TGGAA

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCTCATCCTC TGCTTCTGGT ACG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGATGTACC GTCTGCACA CGAA

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGAGGATCCC AACTTGCCT CTGCTTTTGT GTGG

34

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTCAGTGAA GGGAATGGGA GCGA

24

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTTGCTTGTA CGCCTTCCGG AAGT

24

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGGGCAACAG CCTAGTGATC ACCG

24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTGCTCCCGAG CAGAAGGTCT GGTT

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGAATGGCT CCGGCAGCCA GGG

23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTGGAGACCA GAGCGTAAAC GATGG

25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGATGGCTGA CATCCAGAAC ATTCGCTGG ACAGCCCAGG GAGCG

45

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATCACAGGCA CTGCCACAGC CCCTACGCTC CCTGGGCTGT CCAGCG

46

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGCCAGGCAT CCAGCGTGTA GAT

23

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACGGTCGCTT CGCCTTCAGC CCGCCACCT ACGCCTGTCTG CCTGG

45

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACGGTCGCTT CGCCTTCAGC CCGGCCACCT ACGCCTGTCG CCTGG

45

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCGCAACGCG CGCGCCGCCG TGGGGCTCGT GTGGCTGCTG GCGGC

45

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTACACGC TGGATGCCTG GCTCTTTGGG GCCCTCGTCT GCAAG

45

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATCTACACGC TGGATGCCCT GGCT

24

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGTAGCGCAC GGTGCCGTAG TA

22

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGATCCG CCACCATGGC TGATGCCAG AACATTTAC

40

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGGTACCT GTCCACGGAG ACAGCAGC

28

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGGCTGAT GCCCAGAACA TTCTACTGGA CAGCCCAGGG AGTGT

45

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GACCACAGGC ACTGCCACGG CCCCCACACT CCCTGGGCTG TCCAG

45

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGCAGCCTGG CCCAAGTGCC TGGCAGGAGC CAAGCAGTAC CACAG

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGCGGATCCA TTATGTCTGC ACTCCGAAGG AAATTTG

37

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGCGAATTCT TATGTGAAGC GATCAGAGTT CATTTTTTC

38

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCGGGATCCG CTATGGCTGG TGATTCTAGG AATG

34

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGAATTCC CCTCACACCG AGCCCCTGG

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCAAGCTTCT AATACGACTC ACTATAGGGC CACCATGGCT GATGCCCAGA

50

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTGCAGG GTTATTCCG GTCCTCG

57

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCAGCGGCAC CATGAACGTC TCGGGCT

27

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCCACATCA ACCGTCAGGA TGCT

24

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAGCGCACGG TGCCGTAGTA GCTGAGGT

28

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGAAAGGGT CCCTCCTGCT GCTGCT

26

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TATCAGCTCC ATGCCCTCTA GAAGCC

26

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jonathan A. Bard, et al.
Serial No. : 09/058,333
Filed : April 9, 1998
For : DNA ENCODING GALANIN GALR3 RECEPTOR AND USES
THEREOF

1185 Avenue of the Americas
New York, New York 10036
August 3, 1998

Assistant Commissioner for Patents
Washington, D.C. 20231
Box: Missing Parts

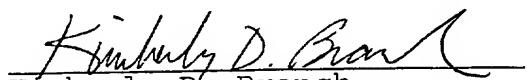
Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(e) and submitted in connection with the above-identified application, has the same information as replacement pages 171-194 of the subject application entitled "Sequence Listing."

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,


Kimberly D. Branch
c/o Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

Applicants: Jonathan A. Bard et al.
Serial No.: Not Yet Known
Filed: Herewith
Exhibit 3

ATCC

10801 University Blvd • Manassas, VA 20110-2209 • Telephone: 703-365-2700 • FAX: 703-

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3
AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

To: (Name and Address of Depositor or Attorney)

Cooper & Dunham LLP
Attn: John P. White, Esq.
1185 Avenue of the Americas
New York, NY 10036

COPY

Deposited on Behalf of: Synaptic Pharmaceutical Corporation (Docket 52241-E)

Identification Reference by Depositor:

ATCC Designation

Plasmid M67

209708

The deposit was accompanied by: ___ a scientific description ___ a proposed taxonomic description indicated above.

The deposit was received March 27, 1998 by this International Depository Authority and has been accepted.

AT YOUR REQUEST: ☒ We will inform you of requests for the strain for 30 years.

The strain will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strain, and ATCC is instructed by the United States Patent & Trademark Office or the depositor to release said strain.

If the culture should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace it with living culture of the same.

The strain will be maintained for a period of at least 30 years from date of deposit, or five years after the most recent request for a sample, whichever is longer. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the culture cited above was tested April 8, 1998. On that date, the culture was viable.

International Depository Authority: American Type Culture Collection, Manassas, VA 20110-2209 USA.

Signature of person having authority to represent ATCC:

Barbara M. Hailey
Barbara M. Hailey, Administrator, Patent Depository

Date: April 22, 1998

cc: Kimberly Branch

Applicants: Jonathan A. Bard et al.
Serial No.: Not Yet Known
Filed: Herewith
Exhibit 4